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Total number of hits satisfying chosen parameters:
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A; Residues: 1-810 < YAM>
A; Cross references: EMBL: AB019195;
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Pred, No. 1.3e-67;
11; Mismatches 219;
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Result No.

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Score

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Minimum Maximum

DB DB

Perfect score: Sequence:

Title:

Scoring table:

Run 옃

Database

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R;McHenry, L.; Fritz, P.J.

Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nuc
A;Reference number: $22477; MUID:92288309
A;Accession: $22477
A;Molecule type: DNA
A;Residues: 1-566 <NCH>
A;Cross·references: EMBL:X62625
A;Cross·references: EMBL:X62625
A;Accession: $22478
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A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted
F;25-566/Product: vicilin #status predicted <MAT>
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A; Residues: 1-452 <MC2>
A; Cross-references: EMBL: X62626
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vicilin precursor - cacao
C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: $22477; $22478; $18105; $22050
C;Accession: $22477; $22778; $1005
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                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 233; Conserv
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IPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAAL
                                                       LRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIR
                                                                                                          ER-GEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPP
                                                                                                                                           GRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL
                                   LKGINDYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVS
                                                                                                                                                                               KEQQRQQEEEL-----QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQ 116
                                                                                                                                                                                                       EEQQREDEEKYEERMKEEDNKRDPQQREYEDCRRRCEQQE--PRQQHQCQLRCREQQRQH 223
                                                                                                                                                                                                                                                      ICEEEEEYNR---QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRY 165
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                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                             Score 1123; DI
Pred. No. 4.5e
08; Mismatches
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A;Recession: $06398
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-globulin type A precursor - upland cotton W;Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1 C;Accession: S06398 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure
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                                   LEANPNTFYLPHHCDAEKIYVYTNGRGTVTFVTHENKESYNVVPGVVVRIPAGSTVYLAN
                                                                   LEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLIN 353
                                                                                                                                        RGGSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVL
                                                                                                                                                                                                                                                      YEKQQQQQPDKQFKECQQRCQWQEQRPERKQQCVKECREQYQEDPWKGER
                                                                                                                                                                                                                                                                                      EEYNRORDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDE 173
                                                                                                                                                                                                                                                                                                                           Q--DKCEDRSETQLKEEQQRDGEDPQRRYQDCRQHCQQEERRLRP-----HCEQSCREQ
                                                                                                                                                                                                                                                                                                                                                            RCVSQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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533-546, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117;
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Pred. No. 4
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A; Molecule type: DNA
A; Residues: 1-81 <CH2>
A; Residues: 1-81 <CH2>
C; Comment: This is a seed storage protein.
C; Superfamily: glycinin
C; Keywords: glycoprotein; seed; storage protein
F; 1-25/Domain: signal seguence #status predicted <SIG>
F; 26-588/Product: alpha-globulin storage proprotein #status predicted
F; 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-globulin B precursor (clone C72) - upland cotton N,Alternate names: seed storage protein; vicilin precursor C;Species: Gossyptum hirsutum (upland cotton) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-J C;Accession: A30838; S06911 R;Cchlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A;Title: Developmental biochemistry of cottonseed embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; A;Experimental source: var. Coker 201 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A;Title: Developmental biochemistry of cottonseed embryogenes A;Reference number: $06398
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A; Residues: 1-588 < CHL>
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A; Accession: A30838
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                                                                                                                                                                                                                                                                                                            EDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQKHC 133
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  EQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT
                                                         FQECQQHCHQQEQRPERKQQCVRECRERYQE-----
                                                                                                                                                               -- RQQEERQRPQCQQRCLKRFEQEQQQ
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                                                                                                                                                                                                                                                                                                                                                                           Score 1082.5;
Pred. No. 1.6e
12; Mismatches
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SO8059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N.Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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                                                                                                   NQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTRSEQLDEL
                                                                                                                                                                                                         ILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLA
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                                                                                                                                                                                                                                                                                                                                                                      ---GSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 292
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Pred. No. 7.8e-57;
Pred. No. 7.8e-57;
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R;Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism
A;Reference number: A53234; MUID:92090707
A;Accession: A53234
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Biochem. Genet. 27, 239-251, 1989
A; Title: Characterization of embryo globulins A; Reference number: A43642; MUID: 89374022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Scaled type: DNA
A; Molecule type: DNA
A; Residues: 1-573 <BEL>
A; Experimental source: inbred line Va 26
A; Experimence extracted from NCBI backbone (NCBIN:71280)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   globulin-15, GLB1S - maize
C;SpecLes: Zea may's (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
R;Belanger, F.C.; Kriz, A.L.
                                                                                                                                                                                                                                                                                                                      В
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                                    YGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPH
                                                                                                FGQ--OREGVIIRASQEQIRELTRDDSE---SRHWHIRRGGESSRGPYNLFNKRPLYSNK 467
                                                                                                                                                                                                                                                                            LLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                      EEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMN-PQRGGSG--
HGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCPH
                                                                              FGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIANQ
                                                                                                                                                            NTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLERL
                                                                                                                                                                                                 NRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGV 412
                                                                                                                                                                                                                                        VLEANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYLA 204
                                                                                                                                                                                                                                                                                                                      EDEREREQEKEEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYRVA 144
                                                                                                                                                                                                                                                                                                                                            ----RYEEGEEEQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 292
                                                                                                                                                                                                                                                                                                                                                                                               EDDNHHHHGGHKSGRCVRRCEDRPWHQRPRCLEQCREEEREKRQERSRHEADDRSGEGSS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHLP----RQSSYEEEEEEEEEEEQEQEEEERRSGQYRKTRSRLSRGDTFVVPANFPVTF
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Pred. No. 1.3e-49;
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K; Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism
A; Reference number: A53234; MUID:92090707
A; Accession: B53234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Glb1-L
A;Introns: 167/1; 225/3;
C;Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vicilin-like storage protein Glb1-L, embryo - maize N;Alternate names: globulin-lL C;Species: Zea mays (maize) C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change C;Accession: B53234; S31824 R;Belanger, F.C.; Kriz, A.L.
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                                                                                                                                                                                                                                                                                                                                                                                    В
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A; Residues: 1-582 <BEL>
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                     NENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIF
                                                                                                                                                                             AYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSG
                                                                                                                                                                                                                              HGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIANQHGQ
                                                                                                                                                                                                                                                                                                       GRKKLVITKILHTISVPGEEQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLERLFGR
                                                                                                                                                                                                                                                                                                                                          NNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQ 415
DSNLQTVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSRREKGF
                                                                            QGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVAVASR
                                                                                                                                                     LYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVCPHRQS
                                                                                                                                                                                                                                                    --QREGVIIRASQEQIRELTRDDSE----SRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQ
                                                                                                                                                                                                                                                                                                                                                                                  ANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYLANTD
                                                                                                                                                                                                                                                                                                                                                                                                                     ANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRD 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDEREQEKEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYRVAVLE
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                                                                                                                -GRGGGKRHEEEEDVH------YEQVRARLSKREAIVVLAGHPVVFVSSG
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RESULT 8
$35221
globulin Beg1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C;Accession: $35221
R;Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D.
"-1 Gen. Genet. 239, 209-218, 1993
"-1 Gen. Genet. 239, 209-218, 1993
"-1 Gen. Genet. 239, 209-218, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 4
C:Superfamily: glycinin
C:Keywords: glycoprotein
F;174-190/Product: globulin Begl #status predicted <MAT>
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A;Title: Barley embryo globulin 1 gene, Begl:
A;Reference number: S35221; MUID:93287988
A;Accession: S35221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-637 <HEC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                               LHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQ----
EESFNSQDQSI-FFPGPRQHQQQSPRSTKQQQ 655
                                          GHPVVEISSSQGSSNLQVVCFEINAERNERVWLAGR-NNVIGKLGSPAQELTFGRPAREV
                                                                    GHPVVFVSS--GNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEV
                                                                                                   RESESEREHGKGRRREEEEDDQRQQRRRGSESESEEEEEQQRYETVRARVSRGSAFVVPP
                                                                                                                                                          LYEADARSFHALANQDVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVQIVCPHL-G
                                                                                                                                                                                    AYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSG
                                                                                                                                                                                                                   EKTRSVSIVRASEEQLRELRREAAEGGQGHRWPLPPFRGDSRDTFNLLEQRPKIANRHGR
                                                                                                                                                                                                                                    ---REGVIIRASQEQIRELTRDDSE---SRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQ
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                                                                                                                                                                                                                                                                                                                                                             AFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNER
                                                                                                                                                                                                                                                                                                                                                                                              ERDEEQGDSRRPYVFGPRSFRRIIQSDHGFVRALRPFDQVSRLLRGIRDYRVAIMEVNPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASHDDEDDRRGGHSLQQCVQRCRQER--PR---YSHARCVQEC-----RDDQQQH- 71
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beta-conglycinin alpha chain precursor - soybean
C;Species: Glycine max (soybean)
C;Date: 07-Mar-1988 #sequence_revision 30-Jun-1991 #text_change
C;Accession: B24810; S16337
R;Doyle, J.J.; Schuler, M.A.; Godette, W.D.; Zenger, V.; Beachy,
J. Biol. Chem. 261, 9228-9238, 1986
A;Title: The glycosylated seed storage proteins of Glycine max a
A;Reference number: A24810; MUID:86250867
A;Accession: B24810
A;Molecule type: DNA
A;Residues: 1-639 <DOY
A;Cross-references: GB:M13759; NID:g169928; PIDN:AAB01374.1; PID
A;Note: the authors translated the codon GGT for residue 352 as a
A;Note: the authors translated the codon GGT for residue 352 as a
A;Title: Closely related families of genes code for the alpha an
A;Reference number: S16337; MUID:83143288
A;Accession: S16337; MUID:83143288
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 361-639 •
C; Genetics:
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                        TKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEED-VHYEQVRARLSKREAIVVLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                  DPQQ--QYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEE
                                                                          SSEDKPFNLGSRDPIYSNKLGKLFEITQRN-PQLRDLDVFLSVVDMNEGALFLPHFNSKA
                                                                                                                 ESSRGPYNLENKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRS
                                                                                                                                                                                                                                     AALNTQTEKLRGVF-----GQQ-----REGVIIRASQEQIRELTRDDSESRHWHIRRGG
                                                                                                                                                                                                                                                                                          NLRMIAGTTFYVVNPDNDENLRMITLAIPVNKPGRFESFFLSSTQAQQSYLQGFSKNILE
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Pred. No. 2.6e-46;
4; Mismatches 221;
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A;Reference number: $20007; MUID:92119248
A;Accession: $20007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-605 <LEL>
C;Superfamily: glycinin
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                                                                                                                                                 QRLQESVIVEISKEQIRALSKRAKSSS----RKTISSEDKPFNLRSRDPIYSNKLGKFFE
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AQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSP
                                                         GRGGGK-----RHEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGIN
                                                                                       ITPEKNPOLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELV------
                                                                                                                   VKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHG
                                                                                                                                                                                                             LAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSREEGQQQGE
                                                                                                                                                                                                                                                                    THLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAK
                                                                                                                                                                                                                                                                                                                                              EEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEQCQKHCQRRETE-PRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEED 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLKVEKEECEEGEIPRPRPRPRPQHPEREPQQPGE-----KEEDEDEQPRPIPFPRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSIL
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                                                                                                                                                                              QR--EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE
                                                                                                                                                                                                                                        FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF-----
                                                                                                                                                                                                                                                                                                                               RHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNSKPNTLLLP
                                                                                                                                                                                                                                                                                                                                                                                         FPRPPHQKE----ERKQEEDED------EEQQRESEESED------SELR
                                                                                                                                                                                                                                                                                                                                                                                                                     NKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRD----PQQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLGLVFLASVSVSFGIAYWEKENPKHNKCLQSCNSERDSYRNQACHARC-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPVMV--NATSDLNFFAFGINAENNQRNFLAGSKDNVISQIPSQVQELAFPRSAKDIENL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVVLVINEGEANIELV------GIKEQQQRQQQEEQPLEVRKYRAELSEQDIFVIPAG
                              -GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV--NATSNLNFFAIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%; Score 842.5; 30.6%; Pred. No. 1.8
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nes 223;
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Best Local :
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RyShutov, A.D.; Kakhovskaya, I.A.; Bastrygina, A.S.; Bulmaga, V.P.; Horstmann, C.; Mu Eur. J. Biochem. 241, 221-228, 1996

A; Title: Limited proteolysis of beta-conglycinin and glycinin, the 7S and 11S storage A; Reference number: S74123; MUID:97054613

A; Reference number: S74124

A; Rolecule type: protein

A; Residues: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4

A; Experimental source: seed

C; Repwords: glycinin

C; Keywords: glycinin; seed; storage protein

C; Keywords: glycoprotein; seed; storage protein

F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-605/Product: beta-conglycinin alpha chain #status predicted <MAT>

F;261,517/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sebastiani, F.L.; Farrell, L.B.; Schuler, M. Plant Mol. Biol. 15, 197-201, 1990
A;Title: Complete sequence of a cDNA of alpha A;Reference number: S14681; MUID:91355860
A;Accession: S14681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-605 <SEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 205; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLFLLSTTVS--LAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDID
                                                                                                                                                                                                                                                                                                   THLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAK
                                                                 QR--EGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE 473
                                                                                                                                  LAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSREEGQQQGE
                                                                                                                                                                                                                                                                                                                                                                                                       RHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNSKPNTLLLP
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QRLQESVIVEISKEQIRALSKRAKSSS----
                                                                                                                                                                                            FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF---
                                                                                                                                                                                                                                                                 NHADADYLIVILNGTAILSLVNNDDRDSYRLQSGDALRVPSGTTYYVVNPDNNENLRLIT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLP 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLGLVFLASVSVSFGIAYWEKENPKHNKCLQSCNSERDSYRNQACHARC-----N
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Pred. No. 2.4e-45;
4; Mismatches 223;
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   RKTISSEDKPFNLRSRDPIYSNKLGKFFE
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V.P.; Hors
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R;Bown, D.; Ellis, T.H.N.; Gatehouse, J.A.
Biochem. J. 251, 717-726, 1988
A;Title: The sequence of a gene encoding convicilin from the sequence of the sequenc
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c;Species: pisum sativum (garden pea)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C;Accession: S00566
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Best Local Similarity
Matches 211; Conserv
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                                                                                                         DAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLFLLSTTVSLAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDW-
                                                                                                                                                                                                         NPYYFDERSLSTRERTEEGHISVLENEYGRSKLLRALKNYRLVLLEANPNAEVLPTHLDA
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                              STPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVF--
                                                                             DLILVVLNGKAILTVLSPNDRNSYNLERGDTIKIPAGTTSYLVNQDDEEDLRVVDFVIPV
                                                                                                                                                                               NPFLFKSNKFLTLFENENGHIRRLQRFDKRSDLFENLQNYRLVEYRAKPHTIFLPQHIDA
                                                                                                                                                                                                                                                                                                                             QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQSD
                                                                                                                                                                                                                                                                                                                                                                                   ----KEVQPG----
                                                                                                                                                                                                                                                                                                                                                                                                                               QKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSYEKEEHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRDPQQQYEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFLGIIFLASVCVTYA-----NYDEGS----ETRVPGQRERGRQEGEKEEKRHGEWR
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                                                                                                                                                                                                                                                                                                                                                                              ----RERWERE----
                                                                                                                                                                                                                                                                              ----ARLRHREERTKRDR-----RHQREGEEEERSSESQEHR
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3.5e-44;
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A;Title: A 62-kD sucrose binding protein is expressed and localized A; Reference number: JQ1730; MUID:93104680
A;Accession: JQ1730
A;Molecule type: mRNA
A;Residues: 1-524 <GRI>
A;Cross-references: GB:L06038; NID:91431744; PIDN:AAB03894.1; PID:91
C;Superfamily: 91yclnin
C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted <NAT
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Best Local S
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KRPLYSNKYGQAYEVKPEDYRQ--LQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVVASG
                                                                                                                                                                                                         RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE
                                                                                                                                                                                                                                                                         LLQGIENFRLAILEARAHTFVSPRHFDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI 200
                                                                          AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS
                                                                                                                         AALNTQTEKLRGVFGQQREGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFN 459
                                                                                                                                                                          HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCKEICEEEEEYNRQRDPQ--QQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQ 162
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A; Retaus: preliminary: translated from GB/EMBL/DDBJ
A; Residues: 1-483 <ROD>
A; Residues: 1-483 <ROD>
A; Residues: 1-483 <ROD>
A; Residues: 1-483 <ROD>
A; Reperimental source: var. Lincoln
C; Superimental source: var. Lincoln
C; Accession: T06459
R; Rodrigo II, M.I.
A; Reference number: 215693
A; Reference number: 215693
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Cross-references: EMBL: Y11207; PIDN: CAA72090.1
A; Experimental source: var. Lincoln
C; Genetics:
A; Note: p54
C; Superfamily: glycinin
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   QAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQ 646
                                                                                                      LANITKGSMSTIHYNTNANKIALVIDGEGELEMACPHMPS-----SSSNSRQKKSSISYH
                                                        NINAKLRPGVMFVVPAGHPFVNIASKKKNLIVVCFEVNAQRNKKLALAGK-KNIVSALDK
                                                                                                                                      IANVTQGSMMGPFFNTRSTKVVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEDVHYE
                                                                                                                                                                        LAPKKS----LWPF----GGPFKSPFNIFSNNPAFSNKFGSLFEVGPSQEKSGLEGLNLMLT
                                                                                                                                                                                               LTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQ-LQDMDLSVF
                                                                                                                                                                                                                                         PVNLEPFFESAGRKPESVLNTFSSKVLQAALKSSKGELETVLDEQKKGRIFKIEKEDVRG
                                                                                                                                                                                                                                                             PGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGVIIRASQEQIRE 431
                                                                                                                                                                                                                                                                                                               NIKGRGIIGLVAEDRTERFNLEEGDIMRVPAGTPMYLVNRDENEKLYIAAFHMPPSSGSA
                                                                                                                                                                                                                                                                                                                                VIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF---LQTIST
                                                                                                                                                                                                                                                                                                                                                                                EDNDFETKIDTKDGRVLILNKFNEKSKLLKNIENYGLAVLEIKANAFLSPHHYDSEAILF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICMERCODYIKKKQE-----RQKHKEH------EEEEEQEQEEDENPYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQSDNPYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDNKRDPQQREY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DERSLSTRERTEEGHISVLENEYGRSKLLRALKNYRLVLLEANPNAEVLPTHLDADAILL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKEKDP-ELTTCKDQCD------MQRQYDEEDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENLLMICFEVNARDNKKFTFAGKD-NIVSSLDNVAKELAFNYPSEMVNGVFLLQRFLERK 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGHLQISCPHMS----SRSSHSKHDKSSP-SYHRISSDLKPGMVFVVPPGHPFVTIASNK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EADVEMACPHLSGRHGGRGGGKRHEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.7%; Score 769.5; DB 2; 31.4%; Pred. No. 5.2e-41; ative 114; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Job time: 538 sec

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RESULT 15
$24756
$24756
$24756
vicilin-like storage protein precursor - white spruce
C;Species: Picea glauca (white spruce)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: $24756; $18873
R;Newton, C.H.; Flinn, B.S.; Sutton, B.C.S.
Plant Mol. Biol. 20, 315-322, 1992
A;Title: Vicilin-like seed storage proteins in the gymnosperm interior spruce (I A;Reference number: $24756; MUID:93004485
A;Accession: $24756
A;Accession: $24756
A;Molecule type: mRNA
A;Residues: 1-448 <NEW>
A;Cross-references: EMBL:X63191; NID:920500; PIDN:CAA44873.1; PID:920501
C;Superfamily: vicilin
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Best Local S
Matches 162
439
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                                                                                                                                                                                                                                             YSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEM
                                                                                                                                                                                                                                                                                                                        GVFGQQREGVIIRASQEQIRELTRDDSESRHWHIRRG---GESSR----GPYNLENKRPL 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAKEVAFDIAAEKVDEVFERKEE-FFFPYDNEERKE
                                 HQQQSPRST
                                                                                                            AFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPR-KEVEESFNSQDQSIFFPGPRQ 642
                                                                                                                                                                                  ACPHLSGRHGGRGGGKRHEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLF
                                                                                                                                                                                                                          FENENGRETTAGPKNYPFLDALDVSVGLADLNPGSMTAPSLNSKSTSIGIVTNGEGRIEM
                                                                                                                                                                                                                                                                                                  RIFGGHKSGVIIHANEEQIREMMR-----KRGFSAGSMSAPEHPKPFNLRNQKPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCIEMKPNTVMLPHYIDATWILYVTRGRGYIAYVHQNELVKRKLEEGDVFGVPSGHTFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYL
RSRDEARSS
                                                                      WFDLNTRGNERQFLAGK-NNVLNTLEREIRQLSFNVPRGEEIEEVLQAQKDQVILRGPQR
                                                                                                                                               ACPHL-GQHG--WSSPRERGDQDITYQRVWAKLRTGSVYIVPAGHPITEIASTNSRLQIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEYLGRGRGRR-EEEREENPYVFHSDSFRTRASSEAGEIRALPNFGEVSELLEGIRKFRV 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 752; DB 1;
Pred. No. 5.9e-40;
5; Mismatches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gymnosperm interior spruce (Picea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448;
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